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<110> Zoghbi, Huda
Ben-Arie, Nissim
Bellen, Hugo
Birmingham, Nessim
Hassan, Bassem

<120> COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN ATONAL-
ASSOCIATED SEQUENCE FOR DEAFNESS, OSTEOARTHRITIS, AND ABNORMAL CELL
PROLIFERATION

<130> HO-P01899US2/09906355/OTA 99-47

<140> US 09/585,645

<141> 2000-06-01

<150> US 60/137,060

<151> 1999-06-01

<150> US 60/176,993

<151> 2000-01-19

<150> PCT/US00/15410

<151> 2000-06-01

<160> 69

<170> PatentIn version 3.0

<210> 1

<211> 1065

<212> DNA

<213> HUMAN

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 35 40 45
 Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp
 50 55 60
 Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
 65 70 75 80
 Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
 85 90 95
 Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly
 100 105 110
 Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
 115 120 125
 Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg
 130 135 140
 Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg
 145 150 155 160
 Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
 165 170 175
 His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
 180 185 190
 Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
 195 200 205
 Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro
 210 215 220

Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
 225 230 235 240
 Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
 245 250 255
 Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
 260 265 270
 Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
 275 280 285
 Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
 290 295 300
 Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
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 340 345 350
 Ala Ser

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 35 40 45
 Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
 50 55 60
 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
 65 70 75 80
 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
 85 90 95
 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
 100 105 110
 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
 115 120 125
 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
 130 135 140
 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
 145 150 155 160
 Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
 165 170 175
 Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
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Val Phe Ser Asp Phe Leu
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<212> PRT
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			20					25					30		
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			35				40					45			
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Gly	Leu	Met	His	Glu	Cys	Lys	Arg	Arg	Pro	Ser	Arg	Ser	Arg	Ala	Val
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Ser	Arg	Gly	Ala	Lys	Thr	Ala	Glu	Thr	Val	Gln	Arg	Ile	Lys	Lys	Thr
			100					105					110		
Arg	Arg	Leu	Lys	Ala	Asn	Asn	Arg	Glu	Arg	Asn	Arg	Met	His	Asn	Leu
		115					120					125			
Asn	Ala	Ala	Leu	Asp	Ala	Leu	Arg	Glu	Val	Leu	Pro	Thr	Phe	Pro	Glu
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Ile	Trp	Ala	Leu	Thr	Glu	Thr	Leu	Arg	Leu	Ala	Asp	His	Cys	Ala	Gly
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Pro	Gly	Ala	Ala	Leu	Gly	Ala	Ser	Gly	Asp	Ser	Pro	Ser	Pro	Pro	Ser
		195					200					205			
Ser	Trp	Ser	Cys	Thr	Asn	Ser	Pro	Ala	Ser	Ser	Ser	Asn	Ser	Thr	Ser
		210				215						220			
Pro	Tyr	Ser	Cys	Thr	Leu	Ser	Pro	Ala	Ser	Pro	Gly	Ser	Asp	Val	Asp
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Tyr	Trp	Gln	Pro	Pro	Pro	Pro	Glu	Lys	His	Arg	Tyr	Ala	Pro	His	Leu
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<212> DNA
<213> MOUSE

<400> 8

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<400> 9

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Lys	Pro	Glu	Ser	Phe	Pro	Lys	Gln	Val	Val	Leu	Arg	Gly	Lys	Ser	Ile	35	40	45	
Lys	Arg	Ala	Pro	Gly	Glu	Glu	Thr	Glu	Lys	Glu	Glu	Glu	Glu	Glu	Asp	50	55	60	
Arg	Glu	Glu	Glu	Asp	Glu	Asn	Gly	Leu	Ser	Arg	Arg	Arg	Gly	Leu	Arg	65	70	75	80
Lys	Lys	Lys	Thr	Thr	Lys	Leu	Arg	Leu	Glu	Arg	Val	Lys	Phe	Arg	Arg	85	90	95	
Gln	Glu	Ala	Asn	Ala	Arg	Glu	Arg	Asn	Arg	Met	His	Gly	Leu	Asn	Asp	100	105	110	
Ala	Leu	Asp	Asn	Leu	Arg	Lys	Val	Val	Pro	Cys	Tyr	Ser	Lys	Thr	Gln	115	120	125	
Lys	Leu	Ser	Lys	Ile	Glu	Thr	Leu	Arg	Leu	Ala	Lys	Asn	Tyr	Ile	Trp	130	135	140	
Ala	Leu	Ser	Glu	Ile	Leu	Arg	Ile	Gly	Lys	Arg	Pro	Asp	Leu	Leu	Thr	145	150	155	160
Phe	Val	Gln	Asn	Leu	Cys	Lys	Gly	Leu	Ser	Gln	Pro	Thr	Thr	Asn	Leu	165	170	175	
Val	Ala	Gly	Cys	Leu	Gln	Leu	Asn	Ala	Arg	Ser	Phe	Leu	Met	Gly	Gln	180	185	190	
Gly	Gly	Glu	Ala	Ala	His	His	Thr	Arg	Ser	Pro	Tyr	Ser	Thr	Phe	Tyr	195	200	205	
Pro	Pro	Tyr	His	Ser	Pro	Glu	Leu	Ala	Thr	Pro	Pro	Gly	His	Gly	Thr	210	215	220	
Leu	Asp	Asn	Ser	Lys	Ser	Met	Lys	Pro	Tyr	Asn	Tyr	Cys	Ser	Ala	Tyr	225	230	235	240
Glu	Ser	Phe	Tyr	Glu	Ser	Thr	Ser	Pro	Glu	Cys	Ala	Ser	Pro	Gln	Phe	245	250	255	

Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser
 260 265 270
 Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly
 275 280 285
 Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala
 290 295 300
 Met Phe Arg Leu Pro Thr Asp Ser His Phe Pro Tyr Asp Leu His Leu
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Asn

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 <211> 1056
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 <213> MOUSE

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<212> PRT
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<400> 11

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			20					25					30		
Pro	Gln	Pro	Pro	Ala	Thr	Leu	Gln	Ala	Arg	Asp	Leu	Pro	Val	Tyr	Pro
		35					40					45			
Ala	Glu	Leu	Ser	Leu	Leu	Asp	Ser	Thr	Asp	Pro	Arg	Ala	Trp	Leu	Thr
	50					55					60				
Pro	Thr	Leu	Gln	Gly	Leu	Cys	Thr	Ala	Arg	Ala	Ala	Gln	Tyr	Leu	Leu
65					70					75					80
His	Ser	Pro	Glu	Leu	Gly	Ala	Ser	Glu	Ala	Ala	Ala	Pro	Arg	Asp	Glu
				85					90					95	
Ala	Asp	Ser	Gln	Gly	Glu	Leu	Val	Arg	Arg	Ser	Gly	Cys	Gly	Gly	Leu
			100					105					110		
Ser	Lys	Ser	Pro	Gly	Pro	Val	Lys	Val	Arg	Glu	Gln	Leu	Cys	Lys	Leu
			115				120					125			
Lys	Gly	Gly	Val	Val	Val	Asp	Glu	Leu	Gly	Cys	Ser	Arg	Gln	Arg	Ala
	130					135						140			
Pro	Ser	Ser	Lys	Gln	Val	Asn	Gly	Val	Gln	Lys	Gln	Arg	Arg	Leu	Ala
145					150					155					160
Ala	Asn	Ala	Arg	Glu	Arg	Arg	Arg	Met	His	Gly	Leu	Asn	His	Ala	Phe
				165					170					175	
Asp	Gln	Leu	Arg	Asn	Val	Ile	Pro	Ser	Phe	Asn	Asn	Asp	Lys	Lys	Leu
			180					185					190		
Ser	Lys	Tyr	Glu	Thr	Leu	Gln	Met	Ala	Gln	Ile	Tyr	Ile	Asn	Ala	Leu
		195					200					205			
Ser	Glu	Leu	Leu	Gln	Thr	Pro	Asn	Val	Gly	Glu	Gln	Pro	Pro	Pro	Pro
	210					215					220				
Thr	Ala	Ser	Cys	Lys	Asn	Asp	His	His	His	Leu	Arg	Thr	Ala	Ser	Ser
225					230					235					240
Tyr	Glu	Gly	Gly	Ala	Gly	Ala	Ser	Ala	Val	Ala	Gly	Ala	Gln	Pro	Ala
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Pro	Gly	Gly	Gly	Pro	Arg	Pro	Thr	Pro	Pro	Gly	Pro	Cys	Arg	Thr	Arg
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		275					280					285			

Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala
 290 295 300

Gln Lys Asp Leu Ser Pro Ser Leu Pro Gly Gly Ile Leu Gln Pro Val
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Gln Glu Asp Asn Ser Lys Thr Ser Pro Arg Ser His Arg Ser Asp Gly
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Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu Ala Ser
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<210> 12
 <211> 3261
 <212> DNA
 <213> MOUSE

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 gaagaagagg aagaagatgg agataaacct aaaagaagag gtcccaagaa aaagaagatg 240
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<210> 13
<211> 501
<212> DNA
<213> ZEBRA FISH
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<221> misc_feature
<222> (115)..(115)
<223> "n" can be any nucleotide

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gacaacacgg acagggagga ggaggaggag agagaggagg actataacgg gctgccaaag	180
aagaagggtc cccgcaaaaa gaaatccgag ggacgcggtg accgagtcaa aatgcgcogt	240
caggaagcaa acgcgcgtga gcgcagccgc atgcacggtc taaacgacgc gctcgaaagc	300
ctgcgcaaag tcgtgccgtg ctactccaaa acgcagaaac tctccaagat cgaaaccctg	360
gggctgggca agaattacat ttgggctctg tctgagactt tgagcgcagg aaagcgacct	420
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<210> 14
<211> 609
<212> DNA
<213> HUMAN

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aacagaatca cagtgtttca cagacaaaag gaaaggaaaa gaagttctca tacgaaaaga	180
gatttattat tacatagaaa attctcacia tagttgaaac aacttcaga aactagtaaa	240
caccttagat agagttgtgc caattactca gccacaagc atctgctttg tcttaattag	300
acaggggagg tgaatgacca ctgtttattt tcattttcct cattaattat gaaaaactgc	360
atttaattca tcttgcatgtg tgagagattg gctgcgaga tgtaagtcgt aagggaagtg	420
gctgtcggtg ggcaacctga acatggcacc ctgcccaagg ggacccttg gtggcactgc	480

acagtaatgc atgccgtaat tgtaatTTTT accatagtcc aaggTTTctt cttgcttcag 540
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 ggcacactc 609

<210> 15
 <211> 675
 <212> DNA
 <213> HUMAN

<400> 15
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 tgttattcta tgaccagag actgtccaaa atagagactg tactactggc caaaaactac 540
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 caaagctgat gcatagggtc ttgccagcca actacagact tgggtggcagg, ctggtcgcag 660
 ctcaacgaca ggagt 675

<210> 16
 <211> 1476
 <212> DNA
 <213> DROSPHILA

<220>
 <221> misc_feature
 <222> (203)..(203)
 <223> "n" can be any nucleotide

<220>
 <221> misc_feature
 <222> (217)..(217)
 <223> "n" can be any nucleotide

<400> 16
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 gtgcctggcg cgagagagat gacaacaggc gaagtgtagg cgtttcacca ccgagcgaaa 180

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gggagggaaa catatctaac centaagtca cccagntcc tcggggagat ctttggccg 240
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aacttggta gaacggcggg gaaaatatTT gtagaatgca tctcgcgggg gttgaccgta 360
gtcaagtctg gatccgatcg gatcgtttca gttgcaacga aactttcaag ccgcgcggat 420
ctgcaatgag ctactactac tcgtctgcct ccgaggagga tggcagttcc cagtatctgg 480
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<210> 17
<211> 189
<212> PRT
<213> DROSOPHILA

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<400> 17

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Tyr Leu Gly Ser Pro Asn Tyr Asn Leu Thr Gln Leu Pro Pro Val Ser
20          25          30
Gly Gln Asp Tyr Gly Gln Gly Ala Phe Leu Ser Pro Glu Trp Gln Phe
35          40          45

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Leu Asp Ala Ala Gly Gly Thr Gln Thr Glu Leu Gly Pro Ile Met Glu
 50 55 60
 Val Gln Gly Gln His Thr Gln Pro Gln Thr Lys Arg Arg Ser Asn Ser
 65 70 75 80
 Ser Thr Gly Ser Asp Gly Arg Lys Ser Ser Pro Glu Gln Thr Asn Leu
 85 90 95
 Ser Pro Thr Val Gln Lys Arg Arg Arg Gln Ala Ala Asn Ala Arg Glu
 100 105 110
 Arg Lys Arg Met Asn Gly Leu Asn Ala Ala Phe Glu Arg Leu Arg Glu
 115 120 125
 Val Val Pro Ala Pro Ser Ile Asp Gln Lys Leu Ser Lys Phe Glu Thr
 130 135 140
 Leu Gln Met Ala Gln Ser Tyr Ile Leu Ala Leu Cys Asp Leu Leu Asn
 145 150 155 160
 Asn Gly Asp Val Glu Val Asp Ala Ala Ala Tyr Thr Ile Phe Gly Asp
 165 170 175
 Ser Asp Ser Gly Phe Gly Leu Ser Gly Gly Ser Leu Ser
 180 185

<210> 18
 <211> 1074
 <212> DNA
 <213> CHICKEN

<400> 18
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 ccgcctcggt ttccatacga cttggaaaac ccggcaaaga aaagcgacag atttgctgcc 1020
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<210> 19
 <211> 178
 <212> PRT
 <213> CHICKEN

<400> 19

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 Ala Pro Arg Glu Arg Arg Arg Arg Arg Gly Arg Ala Arg Ala Arg Thr
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 Glu Ala Leu Leu His Thr Leu Lys Arg Ser Arg Arg Val Lys Ala Asn
 35 40 45
 Asp Arg Glu Arg Asn Arg Met His His Leu Asn Ala Ala Leu Asp Glu
 50 55 60
 Leu Arg Ser Val Leu Pro Thr Phe Pro Asp Asp Thr Lys Leu Thr Lys
 65 70 75 80
 Ile Glu Thr Leu Arg Phe Ala Tyr Asn Tyr Ile Trp Ala Leu Ser Glu
 85 90 95
 Thr Leu Arg Leu Ala Glu Gln Cys Leu Pro Pro Pro Pro Ala Phe Arg
 100 105 110
 Gly Pro Pro Ala Pro Pro Ser Pro Gly Ser Asp Ala Gly Ser Trp Leu
 115 120 125
 Ser Ser Gly Ser Pro Ala Ala Pro Ser Leu Cys Ala Ser Ala Ser Gly
 130 135 140
 Pro Ser Ser Pro Ala Thr Ser Glu Asp Cys Gly Tyr Val Pro Ser Asp
 145 150 155 160
 Ala Leu Arg Ala Phe Arg Gly Leu Pro Pro Ala Ala Pro Gly Ala Pro
 165 170 175

Cys Arg

<210> 20
 <211> 790
 <212> DNA
 <213> CHICKEN

<400> 20

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<210> 21
 <211> 213
 <212> PRT
 <213> CHICKEN

<400> 21

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			20					25					30		
Ser	Ala	Gly	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Asp	Gly	Arg	Pro	Arg	Arg
		35					40					45			
Leu	Gln	Glu	Gly	Ala	Arg	Arg	Ala	Gly	Arg	Gln	Arg	Gly	Pro	Pro	Arg
	50					55					60				
Ala	Ala	Arg	Thr	Ala	Glu	Thr	Ala	Gln	Arg	Ile	Lys	Arg	Ser	Arg	Arg
65					70					75				80	
Leu	Lys	Ala	Asn	Asn	Arg	Glu	Arg	Asn	Arg	Met	His	Asn	Leu	Asn	Ala
			85					90						95	
Ala	Leu	Asp	Ala	Leu	Arg	Asp	Val	Leu	Pro	Thr	Phe	Pro	Glu	Asp	Ala
			100					105					110		
Lys	Leu	Thr	Lys	Ile	Glu	Thr	Leu	Arg	Phe	Ala	His	Asn	Tyr	Ile	Trp
		115					120					125			
Ala	Leu	Thr	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Ala	Ala	Arg	Leu	Gly	Gly
	130					135					140				

Ala Ala Asp Ala Ala Pro Gly Ala Ala Ala Glu Gly Ser Pro Ser Pro
145 150 155 160

Ala Ser Ser Trp Ser Gly Gly Ala Ser Pro Ala Pro Ser Ala Ser Pro
165 170 175

Tyr Ala Cys Thr Leu Ser Pro Gly Ser Pro Ala Gly Ser Ala Ser Asp
180 185 190

Ala Glu His Trp Pro Pro Pro Arg Gly Arg Phe Ala Pro Pro Pro Pro
195 200 205

Pro His Arg Cys Leu
210

<210> 22
<211> 450
<212> DNA
<213> MOUSE

<400> 22
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<210> 23
<211> 149
<212> PRT
<213> MOUSE

<400> 23

Met Lys Ser Ala Cys Lys Pro His Gly Pro Pro Ala Gly Ala Arg Gly
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Ala Pro Pro Cys Ala Gly Ala Ala Glu Arg Ala Val Ser Cys Ala Gly
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Pro Gly Arg Leu Glu Ser Ala Ala Arg Arg Arg Leu Ala Ala Asn Ala
35 40 45

Arg Glu Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu
50 55 60

Arg Arg Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr
65 70 75 80

Glu Thr Leu Gln Met Ala Leu Ser Tyr Ile Ile Ala Leu Thr Arg Ile

85

90

95

Leu Ala Glu Ala Glu Arg Asp Trp Val Gly Leu Arg Cys Glu Gln Arg
 100 105 110

Gly Arg Asp His Pro Tyr Leu Pro Phe Pro Gly Ala Arg Leu Gln Val
 115 120 125

Asp Pro Glu Pro Tyr Gly Gln Arg Leu Phe Gly Phe Gln Pro Glu Pro
 130 135 140

Phe Pro Met Ala Ser
 145

<210> 24
 <211> 861
 <212> DNA
 <213> MOUSE

<400> 24
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 ctggcacaca cacaccttcc attttttccc aaccgcagga tggcgctca tcccttggat 180
 gcgctcacca tccaagtgtc cccagagaca caacaacctt ttcccgagac ctcggaaccac 240
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<210> 25
 <211> 214
 <212> PRT
 <213> MOUSE

<400> 25

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 35 40 45
 Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
 50 55 60
 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
 65 70 75 80
 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
 85 90 95
 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
 100 105 110
 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
 115 120 125
 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
 130 135 140
 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
 145 150 155 160
 Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
 165 170 175
 Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
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 Val Phe Ser Asp Phe Leu
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 <213> MOUSE

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<400> 27

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 1 5 10 15

Cys Tyr Ser Lys Thr Gln Lys Leu

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<400> 29

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Cys Tyr Ser Lys Thr Gln
 20

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 <211> 263
 <212> PRT
 <213> MOUSE

<400> 31

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			20					25					30		
Met	Ser	Ser	Ser	Ala	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Arg	Arg	Pro
			35				40					45			
Gly	Ser	Ala	Arg	Gly	Gln	Arg	Gly	Ala	Glu	Ala	Glu	Gln	Gly	Val	Gln
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65					70				75					80	
Gly	Leu	Met	His	Glu	Cys	Lys	Arg	Arg	Pro	Ser	Arg	Ser	Arg	Ala	Val
			85						90					95	
Ser	Arg	Gly	Ala	Lys	Thr	Ala	Glu	Thr	Val	Gln	Arg	Ile	Lys	Lys	Thr
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Arg	Arg	Leu	Lys	Ala	Asn	Asn	Arg	Glu	Arg	Asn	Arg	Met	His	Asn	Leu
		115					120					125			
Asn	Ala	Ala	Leu	Asp	Ala	Leu	Arg	Glu	Val	Leu	Pro	Thr	Phe	Pro	Glu
		130				135					140				
Asp	Ala	Lys	Leu	Thr	Lys	Ile	Glu	Thr	Leu	Arg	Phe	Ala	His	Asn	Tyr
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Ile	Trp	Ala	Leu	Thr	Glu	Thr	Leu	Arg	Leu	Ala	Asp	His	Cys	Ala	Gly
			165					170						175	
Ala	Gly	Gly	Leu	Gln	Gly	Ala	Leu	Phe	Thr	Glu	Ala	Val	Leu	Leu	Ser

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195	200	205
Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser		
210	215	220
Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp		
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Tyr Trp Gln Pro Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu		
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 <211> 3541
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 <213> MOUSE

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<210> 33
<211> 330
<212> PRT
<213> MOUSE

<400> 33

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35 40 45
Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Asp Gly
50 55 60
Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
65 70 75 80
Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
85 90 95
Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
100 105 110
Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
115 120 125
Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
130 135 140
Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
145 150 155 160
Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
165 170 175

Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile
 180 185 190
 Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly
 195 200 205
 Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu
 210 215 220
 Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240
 Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255
 Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
 260 265 270
 Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285
 Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
 290 295 300
 Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile
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 Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp
 325 330

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 <212> DNA
 <213> MOUSE

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<210> 35
<211> 515
<212> DNA
<213> CHICKEN

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<210> 36
<211> 151
<212> PRT
<213> CHICKEN

<400> 36

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			20					25					30			
Arg	Met	Glu	Ser	Ala	Ala	Lys	Arg	Arg	Leu	Ala	Ala	Asn	Ala	Arg	Glu	
		35					40					45				
Arg	Arg	Arg	Met	Gln	Gly	Leu	Asn	Thr	Ala	Phe	Asp	Arg	Leu	Arg	Lys	
	50					55					60					
Val	Val	Pro	Gln	Trp	Gly	Gln	Asp	Lys	Lys	Leu	Ser	Lys	Tyr	Glu	Thr	
65				70						75				80		
Leu	Gln	Met	Ala	Leu	Ser	Tyr	Ile	Met	Ala	Leu	Thr	Arg	Ile	Leu	Ala	
			85					90						95		
Glu	Ala	Glu	Arg	Tyr	Ser	Thr	Glu	Arg	Glu	Trp	Ile	Asn	Leu	His	Cys	
			100				105						110			
Glu	His	Phe	His	Pro	Glu	Ser	Tyr	His	His	Tyr	Thr	Gly	Gln	Lys	Val	
	115						120					125				

Ala Thr Asp Ser Asp Pro Tyr Ala Gln Arg Ile Phe Ser Tyr His Pro
 130 135 140

Glu His Phe Gln Ile Ala Asn
 145 150

<210> 37
 <211> 1412
 <212> DNA
 <213> MOUSE

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<210> 38
<211> 263
<212> PRT
<213> MOUSE

<400> 38

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			20					25					30		
Met	Ser	Ser	Ser	Ala	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Arg	Arg	Pro
			35				40					45			
Gly	Ser	Ala	Arg	Gly	Gln	Arg	Gly	Ala	Glu	Ala	Gly	Gln	Gly	Val	Gln
			50			55					60				
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Gly	Leu	Met	His	Glu	Cys	Lys	Arg	Arg	Pro	Ser	Arg	Ser	Arg	Ala	Val
				85					90					95	
Ser	Arg	Gly	Ala	Lys	Thr	Ala	Glu	Thr	Val	Gln	Arg	Ile	Lys	Lys	Thr
			100					105					110		
Arg	Arg	Leu	Lys	Ala	Asn	Asn	Arg	Glu	Arg	Asn	Arg	Met	His	Asn	Leu
			115				120					125			
Asn	Ala	Ala	Leu	Asp	Ala	Leu	Arg	Glu	Val	Leu	Pro	Thr	Phe	Pro	Glu
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Asp	Ala	Lys	Leu	Thr	Lys	Ile	Glu	Thr	Leu	Arg	Phe	Ala	His	Asn	Tyr
145					150					155					160
Ile	Trp	Ala	Leu	Thr	Glu	Thr	Leu	Arg	Leu	Ala	Asp	His	Cys	Ala	Gly
				165					170					175	
Ala	Gly	Gly	Leu	Gln	Gly	Ala	Leu	Phe	Thr	Glu	Ala	Val	Leu	Leu	Ser
			180					185					190		
Pro	Gly	Ala	Ala	Leu	Gly	Ala	Ser	Gly	Asp	Ser	Pro	Ser	Pro	Pro	Ser
			195				200					205			
Ser	Trp	Ser	Cys	Thr	Asn	Ser	Pro	Ala	Ser	Ser	Ser	Asn	Ser	Thr	Ser
			210			215						220			
Pro	Tyr	Ser	Cys	Thr	Leu	Ser	Pro	Ala	Ser	Pro	Gly	Ser	Asp	Val	Asp
225					230					235					240
Tyr	Trp	Gln	Pro	Pro	Pro	Pro	Glu	Lys	His	Arg	Tyr	Ala	Pro	His	Leu
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<210> 39
<211> 938
<212> DNA

<213> ZEBRA FISH

<400> 39

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accacgcgc ctggctggct cccgtgcagg ctggcacctg cgcggcacac gccgaatacc      300
tgctgcactc gcccggtctg agcgcggaag gcgtgtcctc tgcctccaac ttcaggaaga      360
gcagcaagag tcctgtcaaa gtacgcgagc tctgccggct taaaggagct gtgggggcag      420
atgagggcag acagcgggcc ccatccagca aatccaccaa cgtcgtgcag aaacagaggc      480
gaatggctgc caatgcccg gagaggcgaa gaatgcacgg attgaaccac gcgttcgacg      540
agctgcgcag tgtcatccca gcctttgaca acgacaagaa actctccaag tacgaaaccc      600
tgcagatggc ccagatctac atcaacgccc tgtccgactt actacagggc cccggtgcta      660
aagccgaccc gccaaactgc gacctgctgc atgccaacgt gttagaaacg gaccgatctc      720
ccagaggatc accgggcgtc tgtcggagag gcacgggcgt gggttaccg taccagtacg      780
aggacggaac attcaactct ttcattggagc aagacctcca gtcgccctct ggaacgagca      840
agtctggttc ggaggccagt aaagactcgc ctcggtcgaa ccggagtgat ggagaagttc      900
tcgcctcact gaagtgcgag tgagacctgc ccgggcgg      938
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<210> 40

<211> 266

<212> PRT

<213> ZEBRA FISH

<400> 40

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Met Asp Gly Met Ser Thr Asp Thr Arg Glu Val Val Glu Leu Asp Val
1          5          10         15
Gln His Ser Ser Leu Gly Arg Gly Glu Gln Ser Lys Tyr Pro Pro Ala
20        25        30
Leu Ala Leu Met Ala Ser Ser Asp Pro Arg Ala Trp Leu Ala Pro Val
35        40        45
Gln Ala Gly Thr Cys Ala Ala His Ala Glu Tyr Leu Leu His Ser Pro
50        55        60
Gly Ser Ser Ala Glu Gly Val Ser Ser Ala Ser Asn Phe Arg Lys Ser
65        70        75        80
Ser Lys Ser Pro Val Lys Val Arg Glu Leu Cys Arg Leu Lys Gly Ala
85        90        95
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Val Gly Ala Asp Glu Gly Arg Gln Arg Ala Pro Ser Ser Lys Ser Thr
 100 105 110
 Asn Val Val Gln Lys Gln Arg Arg Met Ala Ala Asn Ala Arg Glu Arg
 115 120 125
 Arg Arg Met His Gly Leu Asn His Ala Phe Asp Glu Leu Arg Ser Val
 130 135 140
 Ile Pro Ala Phe Asp Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu
 145 150 155 160
 Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu Ser Asp Leu Leu Gln Gly
 165 170 175
 Pro Gly Ala Lys Ala Asp Pro Pro Asn Cys Asp Leu Leu His Ala Asn
 180 185 190
 Val Leu Glu Thr Asp Arg Ser Pro Arg Gly Ser Pro Gly Val Cys Arg
 195 200 205
 Arg Gly Thr Gly Val Gly Tyr Pro Tyr Gln Tyr Glu Asp Gly Thr Phe
 210 215 220
 Asn Ser Phe Met Glu Gln Asp Leu Gln Ser Pro Ser Gly Thr Ser Lys
 225 230 235 240
 Ser Gly Ser Glu Ala Ser Lys Asp Ser Pro Arg Ser Asn Arg Ser Asp
 245 250 255
 Gly Glu Val Leu Ala Ser Leu Lys Cys Glu
 260 265

<210> 41
 <211> 948
 <212> DNA
 <213> FROG

<400> 41
 atgtcagaga tgggtcaatgt gcatgggtgg atggaggaag cccttagttc ccaggatgag 60
 atgaaggaga ggaatcagtc tgcctatgat atcatttcag gtctatgcca tgaggaaagg 120
 ggcagcattg atggagaaga ggatgatgaa gaagaagagg atggagagaa accaaaaaag 180
 aggggaccca aaaaaaagaa gatgaccaag gctagagtgg agagggttcg tgtccgtaga 240
 gtaaaagcca atgccaggga gcgttcaaga atgcatggac ttaatgatgc cctggaaaat 300
 ttgagaaggg ttatgccttg ctattccaaa acacaaaagt tgtctaaaat tgagactctt 360
 agactggcca gaaactatat atgggcatta tctgatattc tagaacaagg tcaaaatgca 420
 gagggaaagg gctttctgga aatactctgc aaaggtcttt ctgagccaac aagcaactta 480
 gtagctggct gcttgcaact tggacctcag gccatgttct tggataaaca cgaagaaaag 540
 tctcatatat gtgattcctc tcttactggg catacttata attaccagtc ccaggacta 600
 cccagtcctc cttatggtaa cattgatgtt caccacttgc acttgaaacc ctcttctttc 660

aaaccagtaa tggatccttc tgtggtaacc catacactta actgtaccac tccaccatat 720
 gaaggagctc taacacctcc actcagcatc ggtggtaatt tttctttgaa gcaagatagt 780
 tcacccgata tggataaatc atatgcattc aggtccccct atccagctct tgggcttggg 840
 ggatctcatg gacatgogtc acactttcat accagtgttc caaggtatga actaccata 900
 gacatggctt acgagcctta cccacacccat gctatattca ctgaataa 948

<210> 42
 <211> 315
 <212> PRT
 <213> FROG

<400> 42

Met Ser Glu Met Val Asn Val His Gly Trp Met Glu Glu Ala Leu Ser
 1 5 10 15
 Ser Gln Asp Glu Met Lys Glu Arg Asn Gln Ser Ala Tyr Asp Ile Ile
 20 25 30
 Ser Gly Leu Cys His Glu Glu Arg Gly Ser Ile Asp Gly Glu Glu Asp
 35 40 45
 Asp Glu Glu Glu Glu Asp Gly Glu Lys Pro Lys Lys Arg Gly Pro Lys
 50 55 60
 Lys Lys Lys Met Thr Lys Ala Arg Val Glu Arg Phe Arg Val Arg Arg
 65 70 75 80
 Val Lys Ala Asn Ala Arg Glu Arg Ser Arg Met His Gly Leu Asn Asp
 85 90 95
 Ala Leu Glu Asn Leu Arg Arg Val Met Pro Cys Tyr Ser Lys Thr Gln
 100 105 110
 Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Arg Asn Tyr Ile Trp
 115 120 125
 Ala Leu Ser Asp Ile Leu Glu Gln Gly Gln Asn Ala Glu Gly Lys Gly
 130 135 140
 Phe Leu Glu Ile Leu Cys Lys Gly Leu Ser Gln Pro Thr Ser Asn Leu
 145 150 155 160
 Val Ala Gly Cys Leu Gln Leu Gly Pro Gln Ala Met Phe Leu Asp Lys
 165 170 175
 His Glu Glu Lys Ser His Ile Cys Asp Ser Ser Leu Thr Gly His Thr
 180 185 190
 Tyr Asn Tyr Gln Ser Pro Gly Leu Pro Ser Pro Pro Tyr Gly Asn Ile
 195 200 205
 Asp Val His His Leu His Leu Lys Pro Ser Ser Phe Lys Pro Val Met
 210 215 220
 Asp Pro Ser Val Val Thr His Thr Leu Asn Cys Thr Thr Pro Pro Tyr

225		230		235		240
Glu Gly Ala Leu Thr	Pro Pro Leu Ser	Ile Gly Gly Asn Phe	Ser Leu			
	245	250	255			
Lys Gln Asp Ser Ser	Pro Asp Met Asp	Lys Ser Tyr Ala Phe	Arg Ser			
	260	265	270			
Pro Tyr Pro Ala Leu Gly	Leu Gly Gly Ser His	Gly His Ala Ser His				
	275	280	285			
Phe His Thr Ser Val	Pro Arg Tyr Glu Leu	Pro Ile Asp Met Ala Tyr				
	290	295	300			
Glu Pro Tyr Pro His	His Ala Ile Phe Thr	Glu				
305	310	315				

<210> 43
 <211> 1550
 <212> DNA
 <213> MOUSE

<400> 43
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 ctaccgtttg acgagtctgt cgtaatgccc gaatcccaga tgtgcagaaa gtttgctaga 120
 caatgtgagg accagaaaca aattaagaaa ccagagagct ttccaaaaca agttgtcctt 180
 cgaggaaaga gcattaaaag ggcccctgga gaagaaaccg agaaagaaga ggaggaagaa 240
 gacagagagg aagaagatga gaatggcttg tccagaagga gggggctcag gaaaaaaaaa 300
 accaccaaac tacgactgga aagggtcaag ttcaggagac aggaagctaa tgcgcgcgag 360
 aggaaccgga tgcacggcct caatgatgct ctggacaatt tgcgaaaagt ggtcccctgt 420
 tactctaaaa cccaaaaact gtccaaaata gaaactttac gactggccaa aaattacatc 480
 tgggcacttt ctgaaattct gaggattggc aagagaccgg atctgctcac gttcgtccaa 540
 aacttatgca aaggtctttc ccagccaact acaaacttgg tggcaggctg cttacagctc 600
 aacgccagaa gtttctgat gggtcagggt ggggaggctg cccaccacac aaggtoaccc 660
 tactccacat tctaccacc ctaccacagc cctgagctgg ccactcccc agggcatggg 720
 actcttgata attccaagtc catgaaacc tacaattact gcagtgcata tgaatccttc 780
 tatgaaagta cctcccctga gtgtgccagc cctcagtttg aaggtccctt aagtcctccc 840
 ccaattaact ataatgggat attttccctg aagcaagaag aaaccttgga ctatggcaaa 900
 aattacaatt atggcatgca ttactgtgca gtgccacca ggggtcccct tgggcagggt 960
 gccatgttca ggttgcccac cgacagccac ttcccttacg acttacatct gcgcagccaa 1020
 tctctcacta tgcaagatga attaaatgca gtttttcata attaatgagg aaaattaaaa 1080
 taaacagtgg tcattcacct cccactctaa ttaaggcaaa gcagatgctt gtgggctgag 1140

taattggcac aactctatct aaggtgttta ctagtttctg aagtgtgttt caaagattgt 1200
 gaccattttc tatgtcataa taaatccctt ttcgtatgag aacttccttt ccttccctct 1260
 tgtctgtatc acactgtgat tctctctctc tctctctctc tctctctctc tctctctctc 1320
 tcttactggc agaataatttc tttcttggtt tagtttcttt caaattcact taatttggtt 1380
 gaacaagggtg tctaagatgt tgctgaataa agacatgcac acagcatact tcaatgtcta 1440
 tttcagttgt acagttatga tgaaaatgca tgttataaaa atcagatgag taaaatgtgt 1500
 ttataattac taggattcat atatgtatct ctgaaatttt agttttttaa 1550

<210> 44
 <211> 337
 <212> PRT
 <213> MOUSE

<400> 44

Met	Leu	Thr	Leu	Pro	Phe	Asp	Glu	Ser	Val	Val	Met	Pro	Glu	Ser	Gln	1	5	10	15
Met	Cys	Arg	Lys	Phe	Ala	Arg	Gln	Cys	Glu	Asp	Gln	Lys	Gln	Ile	Lys	20	25	30	
Lys	Pro	Glu	Ser	Phe	Pro	Lys	Gln	Val	Val	Leu	Arg	Gly	Lys	Ser	Ile	35	40	45	
Lys	Arg	Ala	Pro	Gly	Glu	Glu	Thr	Glu	Lys	Glu	Glu	Glu	Glu	Glu	Asp	50	55	60	
Arg	Glu	Glu	Glu	Asp	Glu	Asn	Gly	Leu	Ser	Arg	Arg	Arg	Gly	Leu	Arg	65	70	75	80
Lys	Lys	Lys	Thr	Thr	Lys	Leu	Arg	Leu	Glu	Arg	Val	Lys	Phe	Arg	Arg	85	90	95	
Gln	Glu	Ala	Asn	Ala	Arg	Glu	Arg	Asn	Arg	Met	His	Gly	Leu	Asn	Asp	100	105	110	
Ala	Leu	Asp	Asn	Leu	Arg	Lys	Val	Val	Pro	Cys	Tyr	Ser	Lys	Thr	Gln	115	120	125	
Lys	Leu	Ser	Lys	Ile	Glu	Thr	Leu	Arg	Leu	Ala	Lys	Asn	Tyr	Ile	Trp	130	135	140	
Ala	Leu	Ser	Glu	Ile	Leu	Arg	Ile	Gly	Lys	Arg	Pro	Asp	Leu	Leu	Thr	145	150	155	160
Phe	Val	Gln	Asn	Leu	Cys	Lys	Gly	Leu	Ser	Gln	Pro	Thr	Thr	Asn	Leu	165	170	175	
Val	Ala	Gly	Cys	Leu	Gln	Leu	Asn	Ala	Arg	Ser	Phe	Leu	Met	Gly	Gln	180	185	190	
Gly	Gly	Glu	Ala	Ala	His	His	Thr	Arg	Ser	Pro	Tyr	Ser	Thr	Phe	Tyr	195	200	205	

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr
 210 215 220
 Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr
 225 230 235 240
 Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe
 245 250 255
 Glu Gly Pro Leu Ser Pro Pro Pro Ile Asn Tyr Asn Gly Ile Phe Ser
 260 265 270
 Leu Lys Gln Glu Glu Thr Leu Asp Tyr Gly Lys Asn Tyr Asn Tyr Gly
 275 280 285
 Met His Tyr Cys Ala Val Pro Pro Arg Gly Pro Leu Gly Gln Gly Ala
 290 295 300
 Met Phe Arg Leu Pro Thr Asp Ser His Phe Pro Tyr Asp Leu His Leu
 305 310 315 320
 Arg Ser Gln Ser Leu Thr Met Gln Asp Glu Leu Asn Ala Val Phe His
 325 330 335

Asn

<210> 45
 <211> 1393
 <212> DNA
 <213> MOUSE

<400> 45
 aagcttcggt gcacgcgacc tgggtgtgcga tctccgagtg agaggggggag ggtcagagga 60
 ggaaggaaaa aaaatcagac cttgcagaag agactaggaa ggtttttgtt gttgtttgttc 120
 ggggcttata cccttcggtt aactgggttg ccagcacctc ctctaacacg gcacctccga 180
 gccattgcag tgcgatgtcc cgcctgctgc atgcagaaga gtgggctgag gtaaaagagt 240
 tgggggacca ccacgcgccat cccagccgc accacgtccc gccgctgacg ccacagccac 300
 ctgctaccct gcaggcgaga gaccttcccg tctaccggc agaactgtcc ctctggata 360
 gcaccgaccc acgcgccttg ctgactccca ctttgcaggg cctctgcacg gcacgcgccg 420
 ccagtatct gctgcattct cccgagctgg gtgcctccga ggccgcggcg ccccgggacg 480
 aggctgacag ccagggtgag ctggtaagga gaagcggctg tggcggcctc agcaagagcc 540
 ccgggcccgt caaagtacgg gaacagctgt gcaagctgaa ggggtggggtt gtagtggacg 600
 agcttggttg cagccgccag cgagcccctt ccagcaaaca ggtgaatggg gtacagaagc 660
 aaaggaggct ggcagcaaac gcaagggaac ggcgcaggat gcacgggctg aaccacgcct 720
 tcgaccagct gcgcaacggt atcccgtcct tcaacaacga caagaagctg tccaaatatg 780
 agaccctaca gatggcccag atctacatca acgctctgtc ggagttgctg cagactccca 840

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atgtcggaga gcaaccgccg ccgcccacag cttcctgcaa aaatgaccac catcaccttc      900
gcaccgcctc ctcctatgaa ggaggtgcg ggcctctgc ggtagctggg gctcagccag      960
ccccgggagg gggcccgaga cctaccccg cggggccttg ccggactcgc ttctcaggcc     1020
cagcttcctc tgggggttac tcggtgcagc tggacgcttt gcatttccca gccttcgagg     1080
acagggccct aacagcgatg atggcacaga aggacctgtc gccttcgctg cccgggggca     1140
tcctgcagcc tgtacaggag gacaacagca aaacatctcc cagatccac agaagtgcg      1200
gagagttttc cccccactct cattacagtg actctgatga ggccagttag gaaggcaaca     1260
gctccctgaa aactgagaca accaaatgcc cttcctagcg cgcggaagc cccgtgacaa     1320
atatccctgc accctttaat ttttggtctg tggatgatcg tgtagcaac gacttgactt     1380
cggacggctg cag                                                         1393

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<210> 46
<211> 351
<212> PRT
<213> MOUSE

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<400> 46

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Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
1          5          10          15
Gly Asp His His Arg His Pro Gln Pro His His Val Pro Pro Leu Thr
          20          25          30
Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Asp Leu Pro Val Tyr Pro
          35          40          45
Ala Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp Leu Thr
          50          55          60
Pro Thr Leu Gln Gly Leu Cys Thr Ala Arg Ala Ala Gln Tyr Leu Leu
65          70          75          80
His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg Asp Glu
          85          90          95
Ala Asp Ser Gln Gly Glu Leu Val Arg Arg Ser Gly Cys Gly Gly Leu
          100          105          110
Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu Cys Lys Leu
          115          120          125
Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg Gln Arg Ala
          130          135          140
Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg Arg Leu Ala
145          150          155          160
Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala Phe
          165          170          175

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Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu
 180 185 190
 Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu
 195 200 205
 Ser Glu Leu Leu Gln Thr Pro Asn Val Gly Glu Gln Pro Pro Pro Pro
 210 215 220
 Thr Ala Ser Cys Lys Asn Asp His His His Leu Arg Thr Ala Ser Ser
 225 230 235 240
 Tyr Glu Gly Gly Ala Gly Ala Ser Ala Val Ala Gly Ala Gln Pro Ala
 245 250 255
 Pro Gly Gly Gly Pro Arg Pro Thr Pro Pro Gly Pro Cys Arg Thr Arg
 260 265 270
 Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala
 275 280 285
 Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala
 290 295 300
 Gln Lys Asp Leu Ser Pro Ser Leu Pro Gly Gly Ile Leu Gln Pro Val
 305 310 315 320
 Gln Glu Asp Asn Ser Lys Thr Ser Pro Arg Ser His Arg Ser Asp Gly
 325 330 335
 Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu Ala Ser
 340 345 350

<210> 47
 <211> 993
 <212> DNA
 <213> MOUSE

<400> 47
 atggcaaaaa tgtatatgaa atccaaggac atggtggagc tgggtcaacac acaatcctgg 60
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 tatggaatgc tcggaacctt aactgaagag catgacagta ttgaggagga tgaagaagag 180
 gaagaagatg gagataaacc taaaagaaga ggtcccaaga aaaagaagat gactaaagct 240
 cgccttgaaa gattcagggc tcgaagagtc aaggccaatg ctagagaacg gaccoggatg 300
 catggcctga atgatgcctt ggataatctt aggagagtca tgccatgtta ctctaaaact 360
 caaaagcttt ccaagataga gactcttcga ctggcaagga actacatctg ggccttgtct 420
 gaagtcctgg agactggtca gacacttgaa gggaagggat ttgtagagat gctatgtaaa 480
 ggtctctctc aaccacaaag caacctgggt gctggatgcc tccaactggg gcctcaatct 540
 accctcctgg agaagcatga ggaaaaatct tcaatttgtg actctactat ctctgtccac 600
 agcttcaact atcagtctcc agggctcccc agcctcctt atggccatat ggaaacacat 660

tctctccatc tcaagcctca accattttaag agtttgggtg actcttttgg gagccatcca 720
cctgactgca gtaccccccc ttatgagggt ccactcacac caccctgag cattagtggc 780
aacttctcct taaagcaaga cggtccct gatttggaaa aatcctacaa tttcatgcca 840
cattatacct ctgcaagtct aagttcaggg catgtgcatt caactccctt tcagactggc 900
actccccgct atgatgttcc tgtagacctg agctatgatt cctactccca ccatagcatt 960
ggaactcagc tcaatacgat cttctctgat tag 993

<210> 48
<211> 330
<212> PRT
<213> MOUSE

<400> 48

Met Ala Lys Met Tyr Met Lys Ser Lys Asp Met Val Glu Leu Val Asn
1 5 10 15
Thr Gln Ser Trp Met Asp Lys Gly Leu Ser Ser Gln Asn Glu Met Lys
20 25 30
Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr
35 40 45
Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Asp Gly
50 55 60
Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
65 70 75 80
Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
85 90 95
Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
100 105 110
Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
115 120 125
Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
130 135 140
Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
145 150 155 160
Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
165 170 175
Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile
180 185 190
Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly
195 200 205
Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu
210 215 220

Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240
 Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255
 Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
 260 265 270
 Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285
 Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
 290 295 300
 Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile
 305 310 315 320
 Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp
 325 330

<210> 49
 <211> 2264
 <212> DNA
 <213> FROG

<400> 49
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 cctgtcttgt agctggagag ctttgtatcg atgctaagag cactgggtat ctacaaagag 120
 gatcactgca tatgaatgga ataaggagtg ctgctgctac ccaggctggg gtttgttccg 180
 agcccttcaa aacctttttg ccatagaatc actgtgttga catgaagtca gattcaccag 240
 tgcattggga gtccatact gaatgccagt caccatgccc actaagttgc atgccagcca 300
 ggctggaagg ctctaccaag agacgtctgg ctgccaatgc cagggaaaga aggagaatgc 360
 aaggactgaa taccgccttc gatagtctga ggaaagtgt accgcaatgg ggtgaggaca 420
 aaaaactttc caagtatgag actctacaga tggcactgag ctacatcatg gactaagca 480
 ggatcctcac ggaagcagaa agatacagca gaactgatcc aggggaatgg actaaaatgc 540
 actttgatca cattcaggaa gaacagtgcc tcagttatat gggagtgaga tgcccaagag 600
 actgtgatcg ctacctgcc cagacttttt ctactagga taggatgt gagcaacagt 660
 cagcaggcaa ggtactatag acctgaagat agcagtgtat tcctacacac agcagccaat 720
 aatacaggga catttgcac atgggttatt tgtcatgtca ttctgccaa tgcaactgctt 780
 atttcattaa gcacccaaag tcccaggact gggaatatat gtagggcacc ccacgtgatg 840
 cagcccaaag tatgtgctgc tgcaactgat agtgagctgt gggacactgg aaaagcaaag 900
 tgcgctggta ttttgtaaat gaaaatgtca ttatgggtgg catataataa ttacttacac 960
 acagcacagt tatataatct cattgctgtt agaaagcccc tttgtctctt accccccatc 1020


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ctgctttcca tgttactaat gcactggtat cagtgaacat gtagaaggta gtatttatac 1080
attagaaaaa cactgaatgt gcataaacat catttttctc aatatacatt tactatatag 1140
ttcagttggt aagtgtctggt aaacagcagc tgcccacaag ttctgtgcac tgctcatagg 1200
ggaaaggaaa catttttgcc acttgctaga gaatgctaatt tgcattgtac tctgtaatat 1260
tgtcttgtgt ccagggttaag aaaggtctaa attaaaatca ataggaggca taatttacac 1320
atttccctta agctgtaatt ttctggcttt tgtctgcatt ttaatagtgg aaaattacaa 1380
cgtgtataaa attcctactg gtctcattct acttgtttct gtaagacaaa ccctgggtgtg 1440
ttttaagga aaccttaagt aattcttttg aatagtatac atttcttgaa tgtttttttt 1500
ttttttttca atgggcatga gttgtttatt tgtaaacaca gctccaaagt taacagattg 1560
cttgatatctt tcagggtatgc aaatggtatt ttagtctatt ctgggacttt gaaatagaaa 1620
gcaatatgca accctttaga attagaaaaat gtagtacaac ggaacaaatg gtgaatggct 1680
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acttttactg gtgtggttgc gttagaataa taaaatcgga tgttgctaag gttgttacag 1800
tatttctttg cccaggttaa tgcattgacct cccatcttac agagtctcta acacgttgcc 1860
aatgtattgt tatctttcga aaaatgtgga tggaacgtga tcagggtgcaa attcatgcga 1920
ttacctgtg cataattcct ataaaacaga gacaatgtgt agttatagga ggattcacta 1980
cacggatgaa agatcttatt tacaacaggt taggcacaaa aagtcagga ccatgaaaaa 2040
ttgtggccct ttagatttac taaattctgg caccagcca ttgtgatgct gcacctgcac 2100
tcagcaccat attataatcc agcacaaggc agtaagtata aggctcccat actcttctca 2160
ctgataagct tgctagagat gttcccaagg aagcccatgt gctgcccatc ttctgccctt 2220
cctctaggca gcactgctc acatgcggaa tgaaggccca agcg 2264

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<210> 50
<211> 138
<212> PRT
<213> FROG

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<400> 50

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Met Lys Ser Asp Ser Pro Val His Gly Glu Ser His Thr Glu Cys Gln
1           5           10           15

Ser Pro Cys Pro Leu Ser Cys Met Pro Ala Arg Leu Glu Gly Ser Thr
          20           25           30

Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly
          35           40           45

Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly

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50	55	60
Glu Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser		
65	70	75 80
Tyr Ile Met Ala Leu Ser Arg Ile Leu Thr Glu Ala Glu Arg Tyr Ser		
	85	90 95
Arg Thr Asp Pro Gly Glu Trp Thr Lys Met His Phe Asp His Ile Gln		
	100	105 110
Glu Glu Gln Cys Leu Ser Tyr Met Gly Val Arg Cys Pro Arg Asp Cys		
	115	120 125
Asp Arg Tyr Leu Pro Gln Thr Phe Ser His		
	130	135

<210> 51
 <211> 2123
 <212> DNA
 <213> FROG

<400> 51
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 taaaaatgaa ataaggagat actaccacagg ctgggggttta ttttgagtct ttcagaactt 180
 tctagggata gaatatctct gctgacatga agtcagattc accagtgcac agggagtgccc 240
 atactggatg ccagtcacca tgcccactaa ggtgcttgcc agccaggctg gaaggctcta 300
 ccaagagacg tctggctgcc aatgccagag aaaggaggag aatgcaagga ctaaataccg 360
 ccttcgatag tctgaggaaa gttgtaccac aatgggggtga agacaaacaa ctttccaaat 420
 atgagactct gcagatggcg ctgagctaca tcatggcact gagcaggatc ctctcggaag 480
 cagagaggta cagcaggact gatccagagg aatggactaa tattcaatat gatcacattg 540
 aggaggagca gtgcctcagt tatatggagg tgagatgccc aagagactgt gatcggttacc 600
 tgccccagac tttttctcac taggataaga gcaggcaagg tactactgac ctgaagacag 660
 cactgtttta atataatggg tcggttatac agcaccctaat gatacaggga catttgcatc 720
 atgggctatt tgtcatgttg tttttcccaa tgcaatgctt atttccttaa gcaccctacg 780
 ttcaggactg ggtacatatg tagggaaccc caagtgatgc agcccagagg atgcgggtgct 840
 gcaacggatg gcagtttagtg agctgtggaa cactggaaaa gccaaagtga ctgggtatatt 900
 gtgaaaggac atgcaagtta ttatgggttg catataatat ttacctccat acagcacagt 960
 gatataactt cattgcctcc atcataacctg tgtgattata tataaaatgg tagttcctga 1020
 gtcactactt tccatgttac ttatgcaactg ttatcagata acatagagaa agtagtatatt 1080
 atacattaga aaaagtacta tatgtgcata taaattggcg tttaaagcag tctggataaa 1140

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tcattttctg tggactcttt tcttacccca aggagccatt tatagtttaa gtgctgctat 1200
aggcactgct cataagggaa aggaaacatt tttgtcactt gctgataata caaattgcat 1260
tctacaccag aattcttaat taactatact gtctagttaa cagaaaggtc taaattaaaa 1320
tcaacaagag gtataattta catattttac cattttctgg cttctgtctg ctttttgaga 1380
gtggcaaatt acaacgtata taaaattcct acagggtctca atctacttgt tgctgtaaag 1440
acaaaccttg gtgtattttt aaggaaacct taagtaattc ttttggttag tatacatttc 1500
ttaaatatth ttatttgtaa tgggcgtcaa ttgtttatth gtaaacgcag ctccaaaaat 1560
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caatgtactg tatacatgct gacctataag ggctatgtag caaagttggg aaaaagtttt 1740
ccctatcaaa atcactgcag gtttattggt ttgttgcaga tagaataata aaatctgaca 1800
ttgctgatgt gggtaaggta ttttattccc catttaatat cttaatcttt cttcttacac 1860
tgaaaacatt actagcccct tgccaatgta ttcttatctg tcaaattcag gagttcatga 1920
gacttacctg tacataatcc ctatgaaacc aagacaatgt gtggggaata agaggatttg 1980
ctgcacaaat tagggcagag atacatgggc tgactgtgac aaatctcttc ttcttcggag 2040
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cctaacgagg caacttcagc acg 2123

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<210> 52
<211> 138
<212> PRT
<213> FROG

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<400> 52

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Met Lys Ser Asp Ser Pro Val His Arg Glu Ser His Thr Gly Cys Gln
1          5          10          15

Ser Pro Cys Pro Leu Arg Cys Leu Pro Ala Arg Leu Glu Gly Ser Thr
          20          25          30

Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly
          35          40          45

Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly
          50          55          60

Glu Asp Lys Gln Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser
65          70          75          80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Ser Glu Ala Glu Arg Tyr Ser
          85          90          95

Arg Thr Asp Pro Glu Glu Trp Thr Asn Ile Gln Tyr Asp His Ile Glu

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100 105 110
 Glu Glu Gln Cys Leu Ser Tyr Met Glu Val Arg Cys Pro Arg Asp Cys
 115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His
 130 135

<210> 53
 <211> 136
 <212> DNA
 <213> BEETLE

<400> 53
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 agacaagtta taccaagctt ggacgctgac cacaaattga gcaagtttga gactctgcag 120
 atggcccaga cctaca 136

<210> 54
 <211> 45
 <212> PRT
 <213> BEETLE

<400> 54

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Gly Leu Asn Glu Ala
 1 5 10 15

Phe Asp Arg Leu Arg Gln Val Ile Pro Ser Leu Asp Ala Asp His Lys
 20 25 30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
 35 40 45

<210> 55
 <211> 137
 <212> DNA
 <213> BEETLE

<400> 55
 gcggcggaatg cgagggagag gcggaggatg aacagtttga atgacgcctt cgacaggctg 60
 cgggacgtgg tgccgtccct tgggaacgat cggaagctgt ccaagtttga gacacttcag 120
 atggcccaga cctacat 137

<210> 56
 <211> 45
 <212> PRT
 <213> BEETLE

<400> 56

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Ser Leu Asn Asp Ala
 1 5 10 15

Phe Asp Arg Leu Arg Asp Val Val Pro Ser Leu Gly Asn Asp Arg Lys

20

25

30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
 35 40 45

<210> 57
 <211> 1572
 <212> DNA
 <213> HUMAN

<220>
 <221> misc_feature
 <222> (1497)..(1497)
 <223> "n" can be any nucleotide

<220>
 <221> misc_feature
 <222> (1504)..(1504)
 <223> "n" can be any nucleotide

<220>
 <221> misc_feature
 <222> (1526)..(1526)
 <223> "n" can be any nucleotide

<220>
 <221> misc_feature
 <222> (1564)..(1564)
 <223> "n" can be any nucleotide

<400> 57
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 ggagaggagc ggggggagac tgagtggcgc gtgccgcttt ttaaaggggc gcagcgcctt 180
 cagcaaccgg agaagcatag ttgcacgcga cctggtgtgt gatctccgag tgggtggggg 240
 agggctcagg agggaaaaaa aaataagacg ttgcagaaga gacccgaaa gggccttttt 300
 tttggttgag ctggtgtccc agtgctgcct ccgacctga gcgtccgagc ctttgcagtg 360
 caatgtcccg cctgctgcat gcagaagagt gggctgaagt gaaggagttg ggagaccacc 420
 atcgccagcc ccagccgcat catctcccgc aaccgccgcc gccgccgag ccacctgcaa 480
 ctttgaggc gagagagcat ccggtctacc cgctgagct gtccctcctg gacagcaccg 540
 acccacgcgc ctggctggct cccactttgc agggcatctg cacggcacgc gccgccagt 600
 atttgctaca ttccccggag ctgggtgcct cagaggccgc tgcgccccgg gacgaggtgg 660
 acggccgggg ggagctggta aggaggagca gcggcggtgc cagcagcagc aagagccccg 720
 ggccggtgaa agtgcgggaa cagctgtgca agctgaaagg cggggtggtg gtagacgagc 780

tgggctgcag cgcgcaacgg gcccttcca gcaaacaggt gaatggggtg cagaagcaga 840
 gacggctagc agccaacgcc agggagcggc gcaggatgca tgggctgaac cagccttcg 900
 accagctgcg caatgttatc ccgtcgttca acaacgacaa gaagctgtcc aaatatgaga 960
 ccctgcagat ggcccaaatac tacatcaacg ccttgtccga gctgctacaa acgcccagcg 1020
 gaggggaaca gccaccgccc cctccagcct cctgcaaaag cgaccaccac caccttcgca 1080
 ccgcggcctc ctatgaaggg ggcgcgggca acgcgaccgc agctggggct cagcaggctt 1140
 ccggagggag ccagcggccc accccgcccg ggagttgccg gactcgcttc tcagccccag 1200
 cttctgcggg agggctactc gtgcagctgg acgctctgca cttctcgact ttcgaggaca 1260
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 tgcagccagt gcaggaggaa aacagcaaaa cttcgctcgc gtcccacaga agcgacgggg 1380
 aattttcccc ccattcccat tacagtgact cggatgaggc aagttaggaa ggtgacagaa 1440
 gcctgaaaac tgagacagaa acaaaactgc cttttcccag tgcgcgggaa gccccnggt 1500
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 gctncagatg gt 1572

<210> 58
 <211> 354
 <212> PRT
 <213> HUMAN

<400> 58

Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
 1 5 10 15
 Gly Asp His His Arg Gln Pro Gln Pro His His Leu Pro Gln Pro Pro
 20 25 30
 Pro Pro Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Glu His Pro Val
 35 40 45
 Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp
 50 55 60
 Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
 65 70 75 80
 Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
 85 90 95
 Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly
 100 105 110
 Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
 115 120 125
 Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg

130	135	140
Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg		
145	150	155 160
Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn		
	165	170 175
His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp		
	180	185 190
Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile		
	195	200 205
Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro		
	210	215 220
Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr		
	225	230 235 240
Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala		
	245	250 255
Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys		
	260	265 270
Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln		
	275	280 285
Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala		
	290	295 300
Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu		
	305	310 315 320
Gln Pro Val Gln Glu Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg		
	325	330 335
Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu		
	340	345 350

Ala Ser

<210> 59
 <211> 485
 <212> DNA
 <213> CHICKEN

<220>
 <221> misc_feature
 <222> (147)..(147)
 <223> "n" can be any nucleotide

<400> 59	
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aggcggcccc tggcgggggg cgcggcncgc gttccggcgg gagcagcccc gggggagcgc	180

ggggcgggcgg cgggcgcgcg gggcgggcggc ggcgggggccg ggccgcgggc gcaggtgagc 240
 ggcgtgcaga agcagcgggcg gctggcgggcc aacgcgcggg agcgggcgcg gatgcacggg 300
 ctgaaccacg ccttcgacca gctgcgtaat gtcatcccct ccttcaacaa cgacaagaag 360
 ctctccaagt acgagacgct gcagatggcg caaatctaca tcagcgccct cgccgagctg 420
 ctgcacgggc cgcccgcgcc ccccgagccg cccgccaagg ccgagctccg cggggccccc 480
 ttcga 485

<210> 60
 <211> 161
 <212> PRT
 <213> CHICKEN

<400> 60

Pro Leu Leu Gly Pro Asp Gly Ala Ala Ala Ala Ser Pro Pro Ala Gly
 1 5 10 15
 Trp Ala Cys Ala Ala Pro His Ala Cys Pro Pro Arg Arg Arg Ala Thr
 20 25 30
 Cys Cys Pro Pro Thr Arg Arg Thr Arg Arg Pro Val Ala Gly Gly Ala
 35 40 45
 Ala Arg Val Pro Ala Gly Ala Ala Pro Gly Glu Arg Gly Ala Ala Ala
 50 55 60
 Gly Ala Arg Gly Gly Gly Gly Gly Ala Gly Pro Arg Ala Gln Val Ser
 65 70 75 80
 Gly Val Gln Lys Gln Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg
 85 90 95
 Arg Met His Gly Leu Asn His Ala Phe Asp Gln Leu Arg Asn Val Ile
 100 105 110
 Pro Ser Phe Asn Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln
 115 120 125
 Met Ala Gln Ile Tyr Ile Ser Ala Leu Ala Glu Leu Leu His Gly Pro
 130 135 140
 Pro Ala Pro Pro Glu Pro Pro Ala Lys Ala Glu Leu Arg Gly Ala Pro
 145 150 155 160

Phe

<210> 61
 <211> 138
 <212> DNA
 <213> PUFFER FISH

<400> 61

gcggcgaacg cgagggagag gaggagaatg cacggcctga ataaagcgtt tgacgaactg 60

aggagcgtca ttccttcctt ggaaaatgag agaaagctct ccaagtatga cactctccag 120
 atggcccaaa cctacatc 138

<210> 62
 <211> 46
 <212> PRT
 <213> PUFFER FISH

<400> 62

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn Lys Ala
 1 5 10 15
 Phe Asp Glu Leu Arg Ser Val Ile Pro Ser Leu Glu Asn Glu Arg Lys
 20 25 30
 Leu Ser Lys Tyr Asp Thr Leu Gln Met Ala Gln Thr Tyr Ile
 35 40 45

<210> 63
 <211> 1477
 <212> DNA
 <213> DROSOPHILA

<400> 63

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 cgtgccactc gggcgggaacg tgctgccttc tgtggcaact cgtttacctg cccccctacc 180
 tgcctttcag gcccttctga ccgtcgtggt ggatttgtga gtataaatag ggccgaaagg 240
 acgagagacc agtcagaaac ccgccagcac tcgcagcggt cgtatcggtt catccagcaa 300
 cataacacca ccatacagca gcagcaacat gtcgtccagt gagatctatc gctactacta 360
 caagacctcc gaggacttgc agggttcaa gacagccgcc gccgagccgt acttcaatcc 420
 catggcagcc tacaatcccg gcgtgacca ctaccagttc aatggcaaca ccttgccag 480
 cagcagcaac tacttgctcg ccaatggctt catcagcttc gagcaggcca gttccgatgg 540
 ctggatctcc tctcgcggc ctagccaccg atctgagagt cccgagtatg tggatctcaa 600
 taccatgtac aatggaggct gcaacaacat ggccagaac caacaatacg gaatgattat 660
 ggagcagtct gttgtttcca cagcgctgc aattccagtg gcctctctc cggcagtgga 720
 ggtcatgggc tcctccaacg tgggcacttg caaacgatt ccagcctcag cagctccgaa 780
 accgaagcgt agctatacca agaagaacca gccaaagcacc accgccacct ccacaccgac 840
 tgcagctgcy gagtcatctg cctcagtga tctctacacg gaggagttcc agaactttga 900
 ctttgacaac tccgccttgt tcgatgacag cgtcgaggat gacgaggacc tcatgctctt 960
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ccaagatgcc gctgccggag gctctggaaa gaagaggcgt ggcaagcaga tcacaccgt 1080
cgtgaagagg aagcgtcgcc tggccgcca tgcacgtgag cgtcgtcgga tgcagaacct 1140
caaccaggcc ttcgatcgtc tccgccagta ccttcctgt ctgggaaacg atcgccagct 1200
gtccaaacac gagaccctcc aaatggccca gacctacata tccgctctcg gggatctgct 1260
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taagtattat gctgtttatt gtttagttaa ttagcctaaa tggaagacaa tgattaagac 1440
taaggaagac aaaataaaaag caccattaat aatttaa 1477

<210> 64
<211> 312
<212> PRT
<213> DROSOPHILA

<400> 64

Met	Ser	Ser	Ser	Glu	Ile	Tyr	Arg	Tyr	Tyr	Tyr	Lys	Thr	Ser	Glu	Asp
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Leu	Gln	Gly	Phe	Lys	Thr	Ala	Ala	Ala	Glu	Pro	Tyr	Phe	Asn	Pro	Met
			20					25					30		
Ala	Ala	Tyr	Asn	Pro	Gly	Val	Thr	His	Tyr	Gln	Phe	Asn	Gly	Asn	Thr
		35					40					45			
Leu	Ala	Ser	Ser	Ser	Asn	Tyr	Leu	Ser	Ala	Asn	Gly	Phe	Ile	Ser	Phe
	50					55					60				
Glu	Gln	Ala	Ser	Ser	Asp	Gly	Trp	Ile	Ser	Ser	Ser	Pro	Ala	Ser	His
65					70					75					80
Arg	Ser	Glu	Ser	Pro	Glu	Tyr	Val	Asp	Leu	Asn	Thr	Met	Tyr	Asn	Gly
				85					90					95	
Gly	Cys	Asn	Asn	Met	Ala	Gln	Asn	Gln	Gln	Tyr	Gly	Met	Ile	Met	Glu
			100					105					110		
Gln	Ser	Val	Val	Ser	Thr	Ala	Pro	Ala	Ile	Pro	Val	Ala	Ser	Pro	Pro
		115					120					125			
Ala	Val	Glu	Val	Met	Gly	Ser	Ser	Asn	Val	Gly	Thr	Cys	Lys	Thr	Ile
	130					135					140				
Pro	Ala	Ser	Ala	Ala	Pro	Lys	Pro	Lys	Arg	Ser	Tyr	Thr	Lys	Lys	Asn
145					150					155					160
Gln	Pro	Ser	Thr	Thr	Ala	Thr	Ser	Thr	Pro	Thr	Ala	Ala	Ala	Glu	Ser
				165					170					175	
Ser	Ala	Ser	Val	Asn	Leu	Tyr	Thr	Glu	Glu	Phe	Gln	Asn	Phe	Asp	Phe
			180					185					190		

Asp Asn Ser Ala Leu Phe Asp Asp Ser Val Glu Asp Asp Glu Asp Leu
 195 200 205
 Met Leu Phe Ser Gly Gly Glu Asp Phe Asp Gly Asn Asp Gly Ser Phe
 210 215 220
 Asp Leu Ala Asp Gly Glu Asn Gln Asp Ala Ala Ala Gly Gly Ser Gly
 225 230 235 240
 Lys Lys Arg Arg Gly Lys Gln Ile Thr Pro Val Val Lys Arg Lys Arg
 245 250 255
 Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Asn Leu Asn
 260 265 270
 Gln Ala Phe Asp Arg Leu Arg Gln Tyr Leu Pro Cys Leu Gly Asn Asp
 275 280 285
 Arg Gln Leu Ser Lys His Glu Thr Leu Gln Met Ala Gln Thr Tyr Ile
 290 295 300
 Ser Ala Leu Gly Asp Leu Leu Arg
 305 310

<210> 65
 <211> 907
 <212> DNA
 <213> FROG

<400> 65
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 gccgggctct tggccagaga ttacctacta gacagcagcg acccccgcgc ctggctctcc 180
 gccacttccc tgcaaagtcg ccctgagtac gtgctgcacc ccccgggccg ggccggggcg 240
 acaaggtgcg ggaactgtgc aaactgaagg ggctgcggga tgatgatgat gatgaggagg 300
 atgatgagga ggaggaagag agatccgagg ggctgtgcag acacaggggt cccctggca 360
 agggccctgg tggggttcag aagcagagga gactggcagc caatgccagg gagaggagga 420
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 acgacaagaa actctccaaa tacgagaccc tgcagatggc tcagatctac atcaacgccc 540
 tgtccgacct gctgcaggcg cccccgact ccagagatcc cccctgcccg cccacctacc 600
 aactgcattc ggggccagag ccaggttag tccagtctgg cagcatgaga ttctcggaga 660
 cttccccccg acagtcccc ctcagccaat tccaggaggg agctgctccc agaagggaat 720
 aggatctggg cccatcttca tcttctcggg aagacatcgc ccatcttcat cttcggggag 780
 aagacagcaa gacatcgcaa gatctcatcg gactgacggc gaattccggg ctccctatag 840
 tgagtcgtat taatttcgat aagccagctg cattaatgaa tcggccaaac gcgcggggag 900
 aggcgggt 907

<210> 66
<211> 259
<212> PRT
<213> FROG

<400> 66

Met	Ala	Arg	Leu	Leu	His	Gly	Ala	Ala	Thr	Ala	Ala	Asp	Trp	Cys	Glu
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Leu	Lys	Glu	Leu	Pro	Ser	Glu	Ala	Gly	Leu	Leu	Ala	Arg	Asp	Tyr	Leu
		20						25					30		
Leu	Asp	Ser	Ser	Asp	Pro	Arg	Ala	Trp	Leu	Ser	Ala	Thr	Ser	Leu	Gln
		35					40					45			
Ser	Arg	Pro	Glu	Tyr	Val	Leu	His	Pro	Pro	Gly	Arg	Ala	His	Lys	Val
	50					55					60				
Arg	Glu	Leu	Cys	Lys	Leu	Lys	Gly	Leu	Arg	Asp	Asp	Asp	Asp	Asp	Glu
65				70					75						80
Glu	Glu	Asp	Asp	Glu	Glu	Glu	Glu	Glu	Arg	Ser	Glu	Gly	Leu	Cys	Arg
			85						90					95	
His	Arg	Gly	Pro	Pro	Gly	Lys	Gly	Pro	Gly	Gly	Val	Gln	Lys	Gln	Arg
			100					105					110		
Arg	Leu	Ala	Ala	Asn	Ala	Arg	Glu	Arg	Arg	Arg	Met	His	Gly	Leu	Asn
		115					120					125			
His	Ala	Phe	Asp	Gln	Leu	Arg	Asn	Val	Ile	Pro	Ser	Phe	Asn	Asn	Asp
	130					135					140				
Lys	Lys	Leu	Ser	Lys	Tyr	Glu	Thr	Leu	Gln	Met	Ala	Gln	Ile	Tyr	Ile
145				150						155					160
Asn	Ala	Leu	Ser	Asp	Leu	Leu	Gln	Ala	Pro	Pro	Asp	Ser	Arg	Asp	Pro
			165						170					175	
Pro	Cys	Pro	Pro	Thr	Tyr	Gln	Leu	His	Ser	Gly	Pro	Glu	Pro	Arg	Leu
			180					185					190		
Val	Gln	Ser	Gly	Ser	Cys	Met	Arg	Phe	Ser	Gly	Asp	Phe	Pro	Gly	Gln
		195					200					205			
Ser	Pro	Leu	Ser	Phe	Gln	Phe	Gln	Glu	Gly	Ala	Ala	Leu	Ser	Gly	Lys
	210					215					220				
Gly	Ile	Gly	Ser	Ala	Pro	Ser	Ser	Ser	Ser	Gly	Glu	Asp	Ser	Lys	Thr
225					230					235					240
Ser	Pro	Arg	Ser	His	Arg	Ser	Asp	Gly	Glu	Phe	Arg	Ser	Pro	Tyr	Ser
				245					250					255	
Glu	Ser	Tyr													

<210> 67

<211> 19
<212> DNA
<213> SYNTHETIC CONSTRUCT

<400> 67
tgaagctttt ggctttgag

19

<210> 68
<211> 19
<212> DNA
<213> SYNTHETIC CONSTRUCT

<400> 68
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19

<210> 69
<211> 37
<212> DNA
<213> HUMAN

<400> 69
gggggcactg acagtaatgc atgccgtatt cgaagtt

37